

SEQUENCE LISTING

<110> West, James W.
Brandt, Cameron S.
Jaspers, Stephen R.

<120> Production of Homotrimeric Fusion
Proteins

<130> 02-17

<140> 10/684,149
<141> 2003-10-10

<150> 60/417,801
<151> 2002-10-11

<160> 23

<170> FastSEQ for Windows Version 4.0

<210> 1
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> C-myc tag

<400> 1
Glu Gln Lys Leu Ile Ser Glu Glu Asp Leu
1 5 10

<210> 2
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Hemagglutinin A epitope tag

<400> 2
Tyr Pro Tyr Asp Val Pro Asp Tyr Ala
1 5

<210> 3
<211> 1377
<212> DNA
<213> Human

<220>
<221> CDS
<222> (14)...(892)

<400> 3
agc atc cct ga gta atg agt ggc ctg ggc cgg agc agg cga ggt ggc cgg 49
Met Ser Gly Leu Gly Arg Ser Arg Arg Gly Gly Arg
1 5 10

agc cgt gtg gac cag gag gag cgc ttt cca cag ggc ctg tgg acg ggg 97
Ser Arg Val Asp Gln Glu Glu Arg Phe Pro Gln Gly Leu Trp Thr Gly
15 20 25

gtg gct atg aga tcc tgc ccc gaa gag cag tac tgg gat cct ctg ctg 145
Val Ala Met Arg Ser Cys Pro Glu Glu Gln Tyr Trp Asp Pro Leu Leu
30 35 40

ggt acc tgc atg tcc tgc aaa acc att tgc aac cat cag agc cag cgc 193
Gly Thr Cys Met Ser Cys Lys Thr Ile Cys Asn His Gln Ser Gln Arg
45 50 55 60

acc tgt gca gcc ttc tgc agg tca ctc agc tgc cgc aag gag caa ggc 241
Thr Cys Ala Ala Phe Cys Arg Ser Leu Ser Cys Arg Lys Glu Gln Gly
65 70 75

aag ttc tat gac cat ctc ctg agg gac tgc atc agc tgt gcc tcc atc 289
Lys Phe Tyr Asp His Leu Leu Arg Asp Cys Ile Ser Cys Ala Ser Ile
80 85 90

tgt gga cag cac cct aag caa tgt gca tac ttc tgt gag aac aag ctc 337
Cys Gly Gln His Pro Lys Gln Cys Ala Tyr Phe Cys Glu Asn Lys Leu
95 100 105

agg agc cca gtg aac ctt cca cca gag ctc agg aga cag cgg agt gga 385
Arg Ser Pro Val Asn Leu Pro Pro Glu Leu Arg Arg Gln Arg Ser Gly
110 115 120

gaa gtt gaa aac aat tca gac aac tcg gga agg tac caa gga ttg gag 433
Glu Val Glu Asn Asn Ser Asp Asn Ser Gly Arg Tyr Gln Gly Leu Glu

125 130 135 140
cac aga ggc tca gaa gca agt cca gct ctc ccg ggg ctg aag ctg agt 481
His Arg Gly Ser Glu Ala Ser Pro Ala Leu Pro Gly Leu Lys Leu Ser
145 150 155

gca gat cag gtg gcc ctg gtc tac agc acg ctg ggg ctc tgc ctg tgt 529
Ala Asp Gln Val Ala Leu Val Tyr Ser Thr Leu Gly Leu Cys Leu Cys
160 165 170

gcc gtc ctc tgc tgc ttc ctg gtg gcg gtg gcc tgc ttc ctc aag aag 577
Ala Val Leu Cys Cys Phe Leu Val Ala Val Ala Cys Phe Leu Lys Lys
175 180 185

agg ggg gat ccc tgc tcc tgc cag ccc cgc tca agg ccc cgt caa agt 625
Arg Gly Asp Pro Cys Ser Cys Gln Pro Arg Ser Arg Pro Arg Gln Ser
190 195 200

ccg gcc aag tct tcc cag gat cac gcg atg gaa gcc ggc agc cct gtg 673
Pro Ala Lys Ser Ser Gln Asp His Ala Met Glu Ala Gly Ser Pro Val
205 210 215 220

agc aca tcc ccc gag cca gtg gag acc tgc agc ttc tgc ttc cct gag 721
Ser Thr Ser Pro Glu Pro Val Glu Thr Cys Ser Phe Cys Phe Pro Glu
225 230 235

tgc agg gcg ccc acg cag gag agc gca gtc acg cct ggg acc ccc gac 769
Cys Arg Ala Pro Thr Gln Glu Ser Ala Val Thr Pro Gly Thr Pro Asp
240 245 250

ccc act tgt gct gga agg tgg ggg tgc cac acc agg acc aca gtc ctg 817
Pro Thr Cys Ala Gly Arg Trp Gly Cys His Thr Arg Thr Thr Val Leu
255 260 265

cag cct tgc cca cac atc cca gac agt ggc ctt ggc att gtg tgt gtg 865
Gln Pro Cys Pro His Ile Pro Asp Ser Gly Leu Gly Ile Val Cys Val
270 275 280

cct gcc cag gag ggg ggc cca ggt gca taaatggggg tcagggaggg 912
Pro Ala Gln Glu Gly Gly Pro Gly Ala
285 290

aaaggaggag ggagagagat ggagaggagg ggagagagaa agagaggtgg ggagagggga 972
gagagatatg aggagagaga gacagaggag gcagaaaagg agagaaaacag aggagacaga 1032
gagggagaga gagacagagg gagagagaga cagagggaa gagaggcaga gagggaaaga 1092
ggcagagaag gaaagagaca ggcagagaag gagagaggca gagagggaga gaggcagaga 1152

gggagagagg cagagagaca gagagggaga gagggacaga gagagataga gcaggaggc 1212
ggggcactct gagtccccgt tcccaagtca gctgttaggtc gtcatcacct aaccacacgt 1272
gcaataaagt cctcgtgcct gctgctcaca gcccccgaga gcccctccctc ctggagaata 1332
aaacctttgg cagctgcct tcctcaaaaa aaaaaaaaaa aaaaa 1377

<210> 4
<211> 293
<212> PRT
<213> Human

<400> 4
Met Ser Gly Leu Gly Arg Ser Arg Arg Gly Gly Arg Ser Arg Val Asp
1 5 10 15
Gln Glu Glu Arg Phe Pro Gln Gly Leu Trp Thr Gly Val Ala Met Arg
20 25 30
Ser Cys Pro Glu Glu Gln Tyr Trp Asp Pro Leu Leu Gly Thr Cys Met
35 40 45
Ser Cys Lys Thr Ile Cys Asn His Gln Ser Gln Arg Thr Cys Ala Ala
50 55 60
Phe Cys Arg Ser Leu Ser Cys Arg Lys Glu Gln Gly Lys Phe Tyr Asp
65 70 75 80
His Leu Leu Arg Asp Cys Ile Ser Cys Ala Ser Ile Cys Gly Gln His
85 90 95
Pro Lys Gln Cys Ala Tyr Phe Cys Glu Asn Lys Leu Arg Ser Pro Val
100 105 110
Asn Leu Pro Pro Glu Leu Arg Arg Gln Arg Ser Gly Glu Val Glu Asn
115 120 125
Asn Ser Asp Asn Ser Gly Arg Tyr Gln Gly Leu Glu His Arg Gly Ser
130 135 140
Glu Ala Ser Pro Ala Leu Pro Gly Leu Lys Leu Ser Ala Asp Gln Val
145 150 155 160
Ala Leu Val Tyr Ser Thr Leu Gly Leu Cys Leu Cys Ala Val Leu Cys
165 170 175
Cys Phe Leu Val Ala Val Ala Cys Phe Leu Lys Lys Arg Gly Asp Pro
180 185 190
Cys Ser Cys Gln Pro Arg Ser Arg Pro Arg Gln Ser Pro Ala Lys Ser
195 200 205
Ser Gln Asp His Ala Met Glu Ala Gly Ser Pro Val Ser Thr Ser Pro
210 215 220
Glu Pro Val Glu Thr Cys Ser Phe Cys Phe Pro Glu Cys Arg Ala Pro
225 230 235 240
Thr Gln Glu Ser Ala Val Thr Pro Gly Thr Pro Asp Pro Thr Cys Ala
245 250 255
Gly Arg Trp Gly Cys His Thr Arg Thr Thr Val Leu Gln Pro Cys Pro
260 265 270
His Ile Pro Asp Ser Gly Leu Gly Ile Val Cys Val Pro Ala Gln Glu

275 280 285
Gly Gly Pro Gly Ala
290

<210> 5
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> PCR primer

<400> 5
gggcctccag gcccaccagg t 21

<210> 6
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> PCR primer

<400> 6
tcacattgga gccactagga a 21

<210> 7
<211> 56
<212> DNA
<213> Artificial Sequence

<220>
<223> PCR primer

<400> 7
acaggtgtcc aggaaattca tataggccgg ccaccatgga tgcaatgaag agaggg 56

<210> 8
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> PCR primer

<400> 8
accctcaggc atcgaacccg aacccgaacc ggatcc 36

<210> 9
<211> 118
<212> DNA
<213> Artificial Sequence

<220>
<223> PCR primer

<400> 9
gatcggatcc atggccgaaa ctgatcctaa aacagttcaa gaccctacca gcgttgtcca 60
gacgctcctg caagagatcg aagataagtt tcagactatg agcgaccaaa tcatttag 118

<210> 10
<211> 100
<212> DNA
<213> Artificial Sequence

<220>
<223> PCR primer

<400> 10
agaatgcatg acatgagctc caggatagat gaccctgaga aaaatatacg agatttaatg 60
acgcaagctg gtgttggaa gttggaaaggaa agtgggtctta 100

<210> 11
<211> 110
<212> DNA
<213> Artificial Sequence

<220>
<223> PCR primer

<400> 11
gatctagaac cacttccttc caactcttcc acaccagctt gcgtcattaa atctgctata 60
ttttctcaa ggtcatctat cctggagctc atgtcatcga ttctctcaat 110

<210> 12
<211> 108
<212> DNA
<213> Artificial Sequence

<220>
<223> PCR primer

<400> 12
gatttggctcg ctcatagtct gaaacttac ttgcattctc tgcaggagcg tctggactac 60
gctggtaagg tcttgaactg ttttaggatc agtttcggcc atggatcc 108

<210> 13
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> PCR primer

<400> 13
cacacgtacg aagatggatg caatgaagag agg 33

<210> 14
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> PCR primer

<400> 14
ggttagatct cgaacccgaa cccgaaccgg 30

<210> 15
<211> 62
<212> DNA
<213> Artificial Sequence

<220>
<223> PCR primer

<400> 15
ctagaataaa ttttgttaa ctttaagaag gagatata tatggctatg agatcctgcc 60
cc 62

<210> 16
<211> 64
<212> DNA
<213> Artificial Sequence

<220>
<223> PCR primer

<400> 16

tctgtatcag gctgaaaatc ttatctcatc cgccaaaaca ctagtgatgg ttagttgtat 60
ggcc 64

<210> 17

<211> 516

<212> DNA

<213> Artificial Sequence

<220>

<223> TACI-HSBP fragment

<400> 17

atggctatga gatccgtccc cgaagagcag tactgggatc ctctgctggg tacctgcatg 60
tcctgcaaaa ccatttgc aa ccatcagagc cagcgcaccc gtgcagcc tt ctgcaggta 120
ctcagctgcc gcaaggagca aggcaagttc tatgaccatc tcctgaggga ctgcacatc 180
tgtgcctcca tctgtgaca gcaccctaag caatgtcat acttctgtga gaacaagctc 240
aggagcggat ccgggtcggg ttccgggtcg agatccatgg ccgaaactga tcctaaaaca 300
gttcaagacc ttaccagcgt agtccagacg ctccgtcaag agatgcaaga taagttcag 360
actatgagcg accaaatcat tgagagaatc gatgacatga gctccaggat agatgacctt 420
gagaaaaata tagcagattt aatgacgcaa gctgggtgtgg aagagttgga aggaagtgg 480
tctagatccg gtggccatca ccatcaccat cactga 516

<210> 18

<211> 171

<212> PRT

<213> Artificial Sequence

<220>

<223> TACI-HSBP fragment

<400> 18

Met Ala Met Arg Ser Cys Pro Glu Glu Gln Tyr Trp Asp Pro Leu Leu

1 5 10 15

Gly Thr Cys Met Ser Cys Lys Thr Ile Cys Asn His Gln Ser Gln Arg

20 25 30

Thr Cys Ala Ala Phe Cys Arg Ser Leu Ser Cys Arg Lys Glu Gln Gly

35 40 45

Lys Phe Tyr Asp His Leu Leu Arg Asp Cys Ile Ser Cys Ala Ser Ile

50 55 60

Cys Gly Gln His Pro Lys Gln Cys Ala Tyr Phe Cys Glu Asn Lys Leu

65 70 75 80

Arg Ser Gly Ser Gly Ser Gly Ser Arg Ser Met Ala Glu Thr

85 90 95

Asp Pro Lys Thr Val Gln Asp Leu Thr Ser Val Val Gln Thr Leu Leu

100 105 110
Gln Glu Met Gln Asp Lys Phe Gln Thr Met Ser Asp Gln Ile Ile Glu
115 120 125
Arg Ile Asp Asp Met Ser Ser Arg Ile Asp Asp Leu Glu Lys Asn Ile
130 135 140
Ala Asp Leu Met Thr Gln Ala Gly Val Glu Glu Leu Glu Gly Ser Gly
145 150 155 160
Ser Arg Ser Gly Gly His His His His His His
165 170

<210> 19
<211> 480
<212> DNA
<213> Artificial Sequence

<220>
<223> NC-1 fragment

<220>
<221> CDS
<222> (1)...(480)

<400> 19
atg cct gag ggt ttt ata aag gca ggc caa agg ccc agt ctt tct ggg 48
Met Pro Glu Gly Phe Ile Lys Ala Gly Gln Arg Pro Ser Leu Ser Gly
1 5 10 15

acc cct ctt gtt agt gcc aac cag cgg gta aca gga atg cct gtg tct 96
Thr Pro Leu Val Ser Ala Asn Gln Arg Val Thr Gly Met Pro Val Ser
20 25 30

gct ttt act gtt att ctc tcc aaa gct tac cca gca ata gga act ccc 144
Ala Phe Thr Val Ile Leu Ser Lys Ala Tyr Pro Ala Ile Gly Thr Pro
35 40 45

ata cca ttt gat aaa att ttg tat aac agg caa cag cat tat gac cca 192
Ile Pro Phe Asp Lys Ile Leu Tyr Asn Arg Gln Gln His Tyr Asp Pro
50 55 60

agg act gga atc ttt act tgt cag ata cca gga ata tac tat ttt tca 240
Arg Thr Gly Ile Phe Thr Cys Gln Ile Pro Gly Ile Tyr Tyr Phe Ser
65 70 75 80

tac cac gtg cat gtg aaa ggg act cat gtt tgg gta ggc ctg tat aag 288
Tyr His Val His Val Lys Gly Thr His Val Trp Val Gly Leu Tyr Lys

85 90 95

aat ggc acc cct gta atg tac acc tat gat gaa tac acc aaa ggc tac 336
Asn Gly Thr Pro Val Met Tyr Thr Tyr Asp Glu Tyr Thr Lys Gly Tyr
100 105 110

ctg gat cag gct tca ggg agt gcc atc atc gat ctc aca gaa aat gac 384
Leu Asp Gln Ala Ser Gly Ser Ala Ile Ile Asp Leu Thr Glu Asn Asp
115 120 125

cag gtg tgg ctc cag ctt ccc aat gcc gag tca aat ggc cta tac tcc 432
Gln Val Trp Leu Gln Leu Pro Asn Ala Glu Ser Asn Gly Leu Tyr Ser
130 135 140

tct gag tat gtc cac tcc tct ttc tca gga ttc cta gtg gct cca atg 480
Ser Glu Tyr Val His Ser Ser Phe Ser Gly Phe Leu Val Ala Pro Met
145 150 155 160

<210> 20

<211> 160

<212> PRT

<213> Artificial Sequence

<220>

<223> NC-1 fragment

<400> 20

Met Pro Glu Gly Phe Ile Lys Ala Gly Gln Arg Pro Ser Leu Ser Gly
1 5 10 15

Thr Pro Leu Val Ser Ala Asn Gln Arg Val Thr Gly Met Pro Val Ser
20 25 30

Ala Phe Thr Val Ile Leu Ser Lys Ala Tyr Pro Ala Ile Gly Thr Pro
35 40 45

Ile Pro Phe Asp Lys Ile Leu Tyr Asn Arg Gln Gln His Tyr Asp Pro
50 55 60

Arg Thr Gly Ile Phe Thr Cys Gln Ile Pro Gly Ile Tyr Tyr Phe Ser
65 70 75 80

Tyr His Val His Val Lys Gly Thr His Val Trp Val Gly Leu Tyr Lys
85 90 95

Asn Gly Thr Pro Val Met Tyr Thr Tyr Asp Glu Tyr Thr Lys Gly Tyr
100 105 110

Leu Asp Gln Ala Ser Gly Ser Ala Ile Ile Asp Leu Thr Glu Asn Asp
115 120 125

Gln Val Trp Leu Gln Leu Pro Asn Ala Glu Ser Asn Gly Leu Tyr Ser

130 135 140
Ser Glu Tyr Val His Ser Ser Phe Ser Gly Phe Leu Val Ala Pro Met
145 150 155 160

<210> 21
<211> 195
<212> DNA
<213> Artificial Sequence

<220>
<223> HSBP-1 fragment

<220>
<221> CDS
<222> (1)...(195)

<400> 21
atg gcc gaa act gat cct aaa aca gtt caa gac ctt acc agc gta gtc 48
Met Ala Glu Thr Asp Pro Lys Thr Val Gln Asp Leu Thr Ser Val Val
1 5 10 15

cag acg ctc ctg caa gag atg caa gat aag ttt cag act atg agc gac 96
 Gln Thr Leu Leu Gln Glu Met Gln Asp Lys Phe Gln Thr Met Ser Asp
 20 25 30

caa atc att gag aga atc gac atg agc tcc agg ata gat gac ctt 144
Gln Ile Ile Glu Arg Ile Asp Asp Met Ser Ser Arg Ile Asp Asp Leu
35 40 45

gag aaa aat ata gca gat tta atg acg caa gct ggt gtg gaa gag ttg 192
Glu Lys Asn Ile Ala Asp Leu Met Thr Gln Ala Gly Val Glu Glu Leu
50 55 60

gaa 195
Glu
65

<210> 22
<211> 65
<212> PRT
<213> Artificial Sequence

<220>
<223> HSBP-1 fragment

<400> 22

Met Ala Glu Thr Asp Pro Lys Thr Val Gln Asp Leu Thr Ser Val Val
1 5 10 15
Gln Thr Leu Leu Gln Glu Met Gln Asp Lys Phe Gln Thr Met Ser Asp
20 25 30
Gln Ile Ile Glu Arg Ile Asp Asp Met Ser Ser Arg Ile Asp Asp Leu
35 40 45
Glu Lys Asn Ile Ala Asp Leu Met Thr Gln Ala Gly Val Glu Glu Leu
50 55 60
Glu
65

<210> 23

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> RYIRS tag

<400> 23

Arg Tyr Ile Arg Ser
1 5